SAT3 (L34076) or SAT3' or SAT52 (U30298), represented by SEQ ID NO: 1 OR SEQ ID NO: 3, respectively, or an SAT of bacterial origin as defined above. The SAT overexpressed in the cytoplasm can also be a noncytoplasmic plant SAT, for example a chloroplast or mitochondrial SAT. These noncytoplasmic plant SATs, naturally, are expressed in the cytoplasm in the form of a precursor protein comprising a signal for addressing to the cellular compartment, other than the cytoplasm, into which the mature functional SAT is released. In order to overexpress these mature functional SATs in the cytoplasm, their addressing signal is removed. In this case, the SAT protein overexpressed in the cytoplasm is a noncytoplasmic plant SAT, with its signal(s) for addressing to cellular compartments, other than the cytoplasm, removed.

C1

Delete the paragraph at page 10, lines 5 – 24, and insert the following:

C2

According to a specific embodiment of the invention, the noncytoplasmic SAT with its addressing signal removed is SAT1' represented by SEQ ID NO: 5.

Delete the paragraph at page 11, lines 1 – 13, and insert the following:

C3

According to a second embodiment of the invention, the SAT is overexpressed in the mitochondria. The protein is advantageously expressed in the cytoplasm in the form of a signal peptide/SAT fusion protein, the mature functional SAT being released inside the mitochondria. Advantageously, the mitochondrial addressing signal peptide is made up of at least one mitochondrial addressing signal peptide from a plant protein which is located in mitochondria, such as the tobacco ATPase β-F1 subunit signal peptide [[25]

C3

Hemon P. *et al.* 1990, Plant Mol. Biol. 15, 895-904], or the SAT1 signal peptide represented by amino acids 1 to 63 in SEQ ID NO: 8.

Delete the paragraph at page 11, lines 14-16 and insert the following:

C4

According to a specific embodiment of the invention, the mitochondrial SAT is SAT1 (U22964) represented by SEQ ID NO: 8.

Delete the paragraph at page 12, lines 17 – 19, and insert the following:

C5

In this case, the SAT can be a chloroplast SAT of plant origin, such as SAT2 or SAT4, represented by SEQ ID NO: 9 and 11, respectively.

Delete the paragraph at page 13, lines 9 – 24, and insert the following:

C6

In the fusion protein according to the invention, the SAT can be homologous or heterologous to the transit peptide. In the first case, the fusion protein is the SAT2 or the SAT4 protein expressed naturally in the chloroplasts of plant cells. In the second case, the transit peptide can be a transit peptide from an SAT2, represented by amino acids 1 to 32 of SEQ ID NO: 9, or the transit peptide from an SAT4, represented by amino acids 1 to 30 of SEQ ID NO: 11, or alternatively a transit peptide from another protein, which is located in plastids, in particular the transit peptides defined below. Plastid localization protein is understood to mean a protein expressed in the cytoplasm of plant cells in the form of a transit peptide/protein fusion protein, the mature protein being localized in the chloroplast after cleavage of the transit peptide.

Delete the paragraph at page 34, lines 3 – 10, and insert the following:

C7

A gene encoding a putative cytosolic serine acetyltransferase (Z34888 or L34076) represented in **Figure** 4 SEQ ID NO: 1, was isolated by functional complementation of an *Escherichia coli* strain deficient in serine acetyltransferase activity. Analysis of the primary sequence showed the presence of strong similarity with the sequence of the bacterial enzyme (56% homology and 41% identity).

Delete the paragraph at page 34, lines 11 – 14, and insert the following:

C8

The following primers were used to amplify the nucleotide sequence and to clone it into the vector used for transforming tobacco plants:

Oligo 1: 5'GAGAGAGGAT CCTCTTTCCA ATCATAAACC ATGGCAACAT GCATAGACAC ATGC 3' (SEQ ID NO: 13)

Oligo 2: 5'GGCTCACCAG ACTAATACAC TAAATTGTGT TTACCTCGAG AGAGAG 3' (SEQ ID NO: 14)

Delete the paragraph at page 36, line 14-16 and insert the following:

C9

The procedure of Example 3 is repeated, using oligonucleotides 3 and 4 below:

Oligo 3: 5'GAGAGAGGAT CCTCTTATCG CCGCGTTAAT ATGCCACCGG CCGGAGAACTC C 3' (SEQ ID NO: 15)

Oligo 4: 5'GAGCCTTACC AGTCTAATGT AGTATATTTC AACCTCGAGA GAGAG 3' (SEQ ID NO: 16)

Delete the paragraph at page 36, line 17 through page 37, line 8, and insert the following:

C10

A gene is isolated which encodes an acetyltransferase (U 30298), and is represented in **Figure** 5 (SEQ ID NO: 3). Analysis of the primary sequence showed the presence of strong similarity with the sequence of the bacterial enzyme (51.6% homology and 42.6% identity). The N-terminal structure (absence of the conditions necessary for organelle addressing) indicates that this isoform is located in the cytosol. On the other hand, it is given as being cysteine-sensitive [27]. This result differs from the data obtained from pea leaves (and from spinach leaves), in the sense that the cysteine regulation site seams to be confined to the cytosol in *A. thaliana* [27]. Moreover, it would seem that *A. thaliana* has at least two cytosolic isoforms: SAT3 (Example 3) and SAT3' (or U30298, Example 4). Unlike the SAT3 gene, the gene corresponding to **SAT3'** has an intron.

Delete the paragraph at page 37, lines 14-21, and insert the following:

C11

A gene encoding a serine acetyltransferase (L78443), which is represented in **Figure** 6 (SEQ ID NO: 5), was isolated by functional complementation of an *Escherichia coli* strain deficient in serine acetyltransferase activity [12]. Analysis of the primary sequence shows strong similarity with the sequence of the bacterial enzyme (52.7% homology and 39% identity).

Delete the paragraph at page 37, line 22 through page 38, line 1 and insert the following:

The following primers were used to amplify the nucleotide sequence and to clone it into the vector which is used for transforming tobacco plants (in bold characters in **Figure** 3):

C12

Oligo 5: 5'GAGAGAGGAT CCCCTCCTCC TCCTCCTCCT ATGGCTGCGT GCATCGACAC CTG 3' (SEQ ID NO: 17)

Oligo 6: 5'GCTCACCAGC CTAATACATT AAACTTTTTC AGCTCGAGAG AGAG 3' (SEQ ID NO: 18)

Delete the paragraph at page 38, lines 5 – 10, and insert the following:

C13

A second gene is obtained which encodes a putative mitochondrial serine acetyltransferase (U22964), and is represented in **Figure** 7 (SEQ ID NO: 7), by repeating the same procedure, using oligo 7 to replace oligo 5 as the 5' primer.

Oligo 7: 5'GAGAGAGGAT CCGGCCGAGA AAAAAAAAAA ATGTTGCCGG TCACAAGTCG CCG 3' (SEQ ID NO: 19)

Delete the paragraph at page 39, line 27 through page 40, line 8, and insert the following:

C14

A mitochondrial fraction lacking in plastid and in cytosolic contaminants was obtained by using the protocol defined for pea leaf mitochondria [12]. The molecular mass of the polypeptide as revealed by antibodies raised against the peptide [-TKTLHTRPLLEDLDR-] (SEQ ID NO: 5, amino acids 49-63) (see SAT1 amino acid sequence), is of the order of 34,000 daltons, a value which is in agreement with the mass of the protein as obtained using sequence analysis programs for predicting cleavage sites.

Delete the paragraph at page 40, lines 14 - 21, and insert the following:

C15

A gene which encodes a serine acetyltransferase (L78444), represented in **Figure** 8 (SEQ ID NO: 9), was isolated by functional complementation of an *Escherichia coli* strain deficient in serine acetyltransferase activity [12]. Analysis of the primary sequence showed the presence of strong similarity with the sequence of the bacterial enzyme (49.5% homology and 35.4% identity).

Delete the paragraph at page 40, line 22 through page 41, line 1 and insert the following:

C16

The following primers were used to amplify the nucleotide sequence and to clone it into the vector which was used to transform tobacco plants (in bold characters in **Figure** 8):

Oligo 8: 5'GAGAGAGGAT CCGACAAGTT GGCATAATTT ATGGTGGATC TATCTTCCT 3' (SEQ ID NO: 20)

Oligo 9: 5'CCTGTGTGAT TGTCGTGTAG TACTCTAGAA ACTCGAGAGA GAG 3' (SEQ ID NO: 21)

Delete the paragraph at page 41, line 21 through page 42, line 3, and insert the following:

C17

A gene which encodes a serine acetyltransferase (SAT4), represented in **Figure** 9 (SEQ ID NO: 11), was isolated by functional complementation of an *Escherichia coli* strain deficient in serine acetyltransferase activity [12]. Analysis of the primary sequence showed the presence of strong similarity with the sequence of the batecterial enzyme (44.5% homology and 32% identity).

Delete the paragraph at page 42, lines 4 – 8, and insert the following.

The following primers were used to amplify the nucleotide sequence and to clone it into the vector which was for transforming tobacco plants:

C18

Oligo 10: 5'GAGAGAGGAT CCGACAAGTTGG CATAATTTAT GGCTTGTATA AACGGCGAGA ATCGTGATTT TTCTT (SEQ ID NO: 22)

Oligo 11: 5'TACCTCGTAC CACTCAGAAC TCTAGAAACT CGAGAGAGAG3' (SEQ ID NO: 23)

Delete the paragraph at page 43, lines 17 – 21, and insert the following:

C19

To obtain expression of the SAT3 (SEQ ID NO: 1) of Example 2 **in the chloroplast** (**Figure** 11), an extension which allows addressing to this compartment is introduced 5' of the cDNA. For this, the optimized transit peptide previously described is used.

In the Abstract:

Delete the abstract and insert the Abstract submitted herewith.

In the claims:

Please amend the following claims:

C20

2. (amended) Method according to claim 60, characterized in that the serine acetyltransferase which is overexpressed in plant cells is a cysteine-sensitive serine acetyltransferase.